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Sequence Listing was accepted.
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Reviewer: Keisha Douglas
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Application No: 10536802 Version No: 2.1

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<110> Japan Science and Technology Agency
Tsukasa SEYA
Misako MATSUMOTO
Hiroyuki OSHIUMI

<120> Novel Adaptor Protein that Binds to Mammalian Toll-Like Receptor 3, and Gene Thereof

<130> 1035-591 / A211-02/PCT

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Thr Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val
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ctc ctg aag ctg ggc cag gaa act gag gcc agg atc tct cta gag gca 251
Leu Leu Lys Leu Gly Gln Glu Thr Glu Ala Arg Ile Ser Leu Glu Ala
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Leu Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly
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gtg gac agc acc gag gac cca gag gag ccc cca gat gtg tcc tgg gct   347
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gtg gcc cgc ttg tac cac ctg ctg gct gag gag aag ctg tgc ccc gcc   395
Val Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala
                100                 105                 110

tcg ctg cgg gac gtg gcc tac cag gaa gcc gtc cgc acc ctc agc tcc   443
Ser Leu Arg Asp Val Ala Tyr Gln Glu Ala Val Arg Thr Leu Ser Ser
            115                 120                 125

agg gac gac cac cgg ctg ggg gaa ctt cag gat gag gcc cga aac cgg   491
Arg Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg
        130                 135                 140

tgt ggg tgg gac att gct ggg gat cca ggg agc atc cgg acg ctc cag   539
Cys Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln
    145                 150                 155

tcc aat ctg ggc tgc ctc cca cca tcc tcg gct ttg ccc tct ggg acc   587
Ser Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr
160                 165                 170                 175

agg agc ctc cca cgc ccc att gac ggt gtt tcg gac tgg agc caa ggg   635
Arg Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly
                180                 185                 190

tgc tcc ctg cga tcc act ggc agc cct gcc tcc ctg gcc agc aac ttg   683
Cys Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu
            195                 200                 205

gaa atc agc cag tcc cct acc atg ccc ttc ctc agc ctg cac cgc agc   731
Glu Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser
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cca cat ggg ccc agc aag ctc tgt gac gac ccc cag gcc agc ttg gtg   779
Pro His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val
    225                 230                 235

ccc gag cct gtc ccc ggt ggc tgc cag gag cct gag gag atg agc tgg   827
Pro Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp
240                 245                 250                 255

ccg cca tcg ggg gag att gcc agc cca cca gag ctg cca agc agc cca   875
Pro Pro Ser Gly Glu Ile Ala Ser Pro Pro Glu Leu Pro Ser Ser Pro
                260                 265                 270

cct cct ggg ctt ccc gaa gtg gcc cca gat gca acc tcc act ggc ctc   923
Pro Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu
            275                 280                 285

cct gat acc ccc gca gct cca gaa acc agc acc aac tac cca gtg gag   971
Pro Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu
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tgc acc gag ggg tct gca ggc ccc cag tct ctc ccc ttg cct att ctg   1019
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Cys Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu
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gag ccg gtc aaa aac ccc tgc tct gtc aaa gac cag acg cca ctc caa   1067
Glu Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln
320                 325                 330                 335

ctt tct gta gaa gat acc acc tct cca aat acc aag ccg tgc cca cct   1115
Leu Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro
                340                 345                 350

act ccc acc acc cca gaa aca tcc cct cct cct cct cct cct cct cct   1163
Thr Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Pro
            355                 360                 365

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Ser Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro
        370                 375                 380

tcc tcc ctg gaa tca tca tcg gaa cag aaa ttc tat aac ttt gtg atc   1259
Ser Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile
    385                 390                 395

ctc cac gcc agg gca gac gaa cac atc gcc ctg cgg gtt cgg gag aag   1307
Leu His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys
400                 405                 410                 415

ctg gag gcc ctt ggc gtg ccc gac ggg gcc acc ttc tgc gag gat ttc   1355
Leu Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe
                420                 425                 430

cag gtg ccg ggg cgc ggg gag ctg agc tgc ctg cag gac gcc ata gac   1403
Gln Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp
            435                 440                 445

cac tca gct ttc atc atc cta ctt ctc acc tcc aac ttc gac tgt cgc   1451
His Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg
        450                 455                 460

ctg agc ctg cac cag gtg aac caa gcc atg atg agc aac ctc acg cga   1499
Leu Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg
    465                 470                 475

cag ggg tcg cca gac tgt gtc atc ccc ttc ctg ccc ctg gag agc tcc   1547
Gln Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser
480                 485                 490                 495

ccg gcc cag ctc agc tcc gac acg gcc agc ctg ctc tcc ggg ctg gtg   1595
Pro Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val
                500                 505                 510

cgg ctg gac gaa cac tcc cag atc ttc gcc agg aag gtg gcc aac acc   1643
Arg Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr
            515                 520                 525

ttc aag ccc cac agg ctt cag gcc cga aag gcc atg tgg agg aag gaa   1691
Phe Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu
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cgg atg cag gcg gcg gca ctg aac gca gcc tac tca gcc tac ctc cag   1787
Arg Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln
560                 565                 570                 575

agc tac ttg tcc tac cag gca cag atg gag cag ctc cag gtg gct ttt   1835
Ser Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe
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ggg agc cac atg tca ttt ggg act ggg gcg ccc tat ggg gct cga atg   1883
Gly Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met
            595                 600                 605

ccc ttt ggg ggc cag gtg ccc ctg gga gcc ccg cca ccc ttt ccc act   1931
Pro Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr
        610                 615                 620

tgg ccg ggg tgc ccg cag ccg cca ccc ctg cac gca tgg cag gct ggc   1979
Trp Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly
    625                 630                 635

acc ccc cca ccg ccc tcc cca cag cca gca gcc ttt cca cag tca ctg   2027
Thr Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu
640                 645                 650                 655

ccc ttc ccg cag tcc cca gcc ttc cct acg gcc tca ccc gca ccc cct   2075
Pro Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro
                660                 665                 670

cag agc cca ggg ctg caa ccc ctc att atc cac cac gca cag atg gta   2123
Gln Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val
            675                 680                 685

cag ctg ggg ctg aac aac cac atg tgg aac cag aga ggg tcc cag gcg   2171
Gln Leu Gly Leu Asn Asn His Met Trp Asn Gln Arg Gly Ser Gln Ala
        690                 695                 700

ccc gag gac aag acg cag gag gca gaa tgaccgcgtg tccttgcctg         2218
Pro Glu Asp Lys Thr Gln Glu Ala Glu
    705                 710

accacctggg gaacacccct ggacccaggc atcggccagg accccataga gcaccccggt 2278

ctgccctgtg ccctgtggac agtggaagat gaggtcatct gccactttca ggacattgtc 2338

cgggagccct tcatttagga caaaacgggc gcgatgatgc cctggctttc agggtggtca 2398

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Pro Arg Pro Gly Cys Gln Gly Gln Asp Leu Leu His Ala Met Val Leu
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Lys Ala Asp Ala Val Ala Arg Leu Val Ala Arg Gln Trp Ala Gly Val
 65   70   75   80

Asp Ser Thr Glu Asp Pro Glu Glu Pro Pro Asp Val Ser Trp Ala Val
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Ala Arg Leu Tyr His Leu Leu Ala Glu Glu Lys Leu Cys Pro Ala Ser
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Asp Asp His Arg Leu Gly Glu Leu Gln Asp Glu Ala Arg Asn Arg Cys
    130   135   140

Gly Trp Asp Ile Ala Gly Asp Pro Gly Ser Ile Arg Thr Leu Gln Ser
145   150   155   160

Asn Leu Gly Cys Leu Pro Pro Ser Ser Ala Leu Pro Ser Gly Thr Arg
                165   170   175

Ser Leu Pro Arg Pro Ile Asp Gly Val Ser Asp Trp Ser Gln Gly Cys
            180   185   190

Ser Leu Arg Ser Thr Gly Ser Pro Ala Ser Leu Ala Ser Asn Leu Glu
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Ile Ser Gln Ser Pro Thr Met Pro Phe Leu Ser Leu His Arg Ser Pro
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His Gly Pro Ser Lys Leu Cys Asp Asp Pro Gln Ala Ser Leu Val Pro
225   230   235   240

Glu Pro Val Pro Gly Gly Cys Gln Glu Pro Glu Glu Met Ser Trp Pro
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Pro Gly Leu Pro Glu Val Ala Pro Asp Ala Thr Ser Thr Gly Leu Pro
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Asp Thr Pro Ala Ala Pro Glu Thr Ser Thr Asn Tyr Pro Val Glu Cys
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Thr Glu Gly Ser Ala Gly Pro Gln Ser Leu Pro Leu Pro Ile Leu Glu
305                 310                 315                 320

Pro Val Lys Asn Pro Cys Ser Val Lys Asp Gln Thr Pro Leu Gln Leu
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Ser Val Glu Asp Thr Thr Ser Pro Asn Thr Lys Pro Cys Pro Pro Thr
            340                 345                 350

Pro Thr Thr Pro Glu Thr Ser Pro Pro Pro Pro Pro Pro Pro Pro Ser
        355                 360                 365

Ser Thr Pro Cys Ser Ala His Leu Thr Pro Ser Ser Leu Phe Pro Ser
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Ser Leu Glu Ser Ser Ser Glu Gln Lys Phe Tyr Asn Phe Val Ile Leu
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His Ala Arg Ala Asp Glu His Ile Ala Leu Arg Val Arg Glu Lys Leu
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Glu Ala Leu Gly Val Pro Asp Gly Ala Thr Phe Cys Glu Asp Phe Gln
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Val Pro Gly Arg Gly Glu Leu Ser Cys Leu Gln Asp Ala Ile Asp His
        435                 440                 445

Ser Ala Phe Ile Ile Leu Leu Leu Thr Ser Asn Phe Asp Cys Arg Leu
    450                 455                 460

Ser Leu His Gln Val Asn Gln Ala Met Met Ser Asn Leu Thr Arg Gln
465                 470                 475                 480

Gly Ser Pro Asp Cys Val Ile Pro Phe Leu Pro Leu Glu Ser Ser Pro
                485                 490                 495

Ala Gln Leu Ser Ser Asp Thr Ala Ser Leu Leu Ser Gly Leu Val Arg
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Leu Asp Glu His Ser Gln Ile Phe Ala Arg Lys Val Ala Asn Thr Phe
        515                 520                 525

Lys Pro His Arg Leu Gln Ala Arg Lys Ala Met Trp Arg Lys Glu Gln
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Asp Thr Arg Ala Leu Arg Glu Gln Ser Gln His Leu Asp Gly Glu Arg
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Met Gln Ala Ala Ala Leu Asn Ala Ala Tyr Ser Ala Tyr Leu Gln Ser
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Tyr Leu Ser Tyr Gln Ala Gln Met Glu Gln Leu Gln Val Ala Phe Gly
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Ser His Met Ser Phe Gly Thr Gly Ala Pro Tyr Gly Ala Arg Met Pro
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Phe Gly Gly Gln Val Pro Leu Gly Ala Pro Pro Pro Phe Pro Thr Trp
    610                 615                 620

Pro Gly Cys Pro Gln Pro Pro Pro Leu His Ala Trp Gln Ala Gly Thr
625                 630                 635                 640

Pro Pro Pro Pro Ser Pro Gln Pro Ala Ala Phe Pro Gln Ser Leu Pro
                645                 650                 655

Phe Pro Gln Ser Pro Ala Phe Pro Thr Ala Ser Pro Ala Pro Pro Gln
            660                 665                 670

Ser Pro Gly Leu Gln Pro Leu Ile Ile His His Ala Gln Met Val Gln
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Ser Leu Cys Ser Gly Ser Gln Glu Ser Lys Leu Leu His Ala Met Val
             35                  40                  45

ctc ctg gct ctg ggc cag gac acg gag gcc agg gtc tct ctg gag tcc   254
Leu Leu Ala Leu Gly Gln Asp Thr Glu Ala Arg Val Ser Leu Glu Ser
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 80                  85                  90
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